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HUMAN CYCLIN-DEPENDENT KINASE (*hPNQALRE*)

CROSS REFERENCE TO RELATED APPLICATION

This application is a continuation application of U.S. Serial No. 09/464,065 filed December 15, 1999 which claims a priority benefit of provisional application Serial No. 60/112,497 filed December 16, 1998.

TECHNICAL FIELD

The invention relates to the area of protein kinases. More particularly, the invention relates to cyclin-dependent protein kinases.

BACKGROUND OF THE INVENTION

The pathways responsible for regulating mitosis and migration and for transducing environmental stress signals in cells have not been fully described. Such proteins can be manipulated, for example, to protect cells against stress due to disease or environmental conditions and to treat disorders involving alterations in mitosis or migration, such as neoplasia. Thus, there is a need in the art for the identification of proteins which are involved in these pathways.

SUMMARY OF THE INVENTION

The present invention provides, in various embodiments, reagents and methods for diagnosing and treating neoplasia, as well as regulating the cell cycle.

One embodiment of the invention provides isolated polypeptides having at least 223 contiguous amino acids of an hPNQALRE protein selected from the group consisting of SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8. Other related embodiments provide isolated polypeptides comprising amino acid sequences that are at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to amino acids 26-38 and/or amino acids 181-201 of SEQ ID NO:6. Also provided are isolated polypeptides comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8.

Other embodiments of the present invention provide fusion proteins comprising first and second protein segments which are fused together by means of a peptide bond. First proteins of the present invention include, for example, at least 223 contiguous amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8. Also provided are fusion proteins in which the first protein segment comprises an amino acid sequence that is at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to amino acids 26-38 or amino acids 181-201 of SEQ ID NO:6.

Still other embodiments of the present invention include preparations of antibodies that specifically bind to a protein comprising an amino acid sequence of SEQ ID NO:4, SEQ ID NO:6 and/or SEQ ID NO:8. Related embodiments include antibody preparations that specifically bind to an epitope defined in whole or in part by amino acids 26-38 of SEQ ID NO:6 and/or SEQ ID NO:8 and/or amino acids 181-201 of SEQ ID NO:6.

Further embodiments provide cDNA molecules that encode polypeptides comprising at least 223 contiguous amino acids of an hPNQALRE protein selected from the group consisting of SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8. Similar embodiments include cDNA molecules that encode polypeptides comprising an amino acid sequence that is at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to amino acids 26-38 and/or 181-201 of SEQ ID NO:6. The present invention also provides cDNAs that encode polypeptides comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8. Inventive cDNA molecules are also provided that comprise a nucleic acid sequence that is at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to nucleotides 76-114 of SEQ ID NO:5 and/or that is at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to nucleotides 503-564 of SEQ ID NO:3 and/or that is at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to nucleotides 542-603 of SEQ ID NO:5. Also provided are cDNA molecules that

comprise a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:7.

Still further embodiments of the present invention include isolated subgenomic polynucleotides or the complements thereof that comprise a nucleotide sequence that hybridizes under stringent conditions to nucleotides 76-114 of SEQ ID NO:5 and/or nucleotides 503-564 of SEQ ID NO:3.

Other inventive embodiments include constructs comprising a promoter and a polynucleotide segment encoding at least 223 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8. By exemplary constructs, the polynucleotide segment is located downstream from the promoter and transcription of the polynucleotide segment initiates at the promoter. Similar embodiments include constructs comprising a promoter and a polynucleotide segment encoding a polypeptide comprising an amino acid sequence that is at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to amino acids 26-38 and/or amino acids 181-201 of SEQ ID NO:6. The polynucleotide segment may be located downstream from the promoter and transcription of the polynucleotide segment may initiate at the promoter. Inventive constructs also comprise a promoter and a polynucleotide segment encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8.

Other inventive embodiments include host cells that comprise any of the constructs provided herein.

Further embodiments provide homologously recombinant cells that incorporate a new transcription initiation unit. New transcription initiation units of the present invention may comprise an exogenous regulatory sequence, an exogenous exon and a splice donor site. The new transcription initiation unit may be located upstream of the coding sequence of a gene having a coding sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:7. The exogenous regulatory sequence may direct transcription of the coding sequence of the gene.

Still further embodiments provide methods of diagnosing or prognosing neoplasia. Such methods may comprise the step of comparing expression of a first

hPNQALRE gene in a first tissue suspected of being neoplastic with the expression of a second *hPNQALRE* gene of a second tissue that is normal. The first and second *hPNQALRE* genes may comprise coding sequences selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:7. By these methods, over-expression of the first *hPNQALRE* gene in the first tissue indicates neoplasia in the first tissue. By similar methods of diagnosing or prognosing neoplasia, the first and/or second *hPNQALRE* genes may comprise a coding sequence selected from the group consisting of nucleotides 76-114 of SEQ ID NO:5, nucleotides 503-564 of SEQ ID NO:3 and/or nucleotides 542-603 of SEQ ID NO:5.

The present invention thus provides the art with amino acid sequences of hPNQALRE, a unique member of the cyclin-dependent kinase family, and DNA sequences which encode hPNQALRE. The invention can be used, *inter alia*, to treat neoplasia and other proliferative diseases.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 compares the amino acid sequences of the four forms of hPNQALRE.

Figure 2 compares nucleotide coding sequences which encode the four forms of hPNQALRE.

DETAILED DESCRIPTION OF THE INVENTION

A novel human cyclin-dependent kinase termed hPNQALRE is a discovery of the present invention. hPNQALRE is a member of the cyclin-dependent kinase family. hPNQALRE is over-expressed in tumors and can be used both diagnostically and therapeutically.

Amino acid sequences of four forms of human hPNQALRE protein (SEQ ID NOS:2, 4, 6, and 8), as well as polynucleotide sequences which encode the four forms of hPNQALRE (SEQ ID NOS:1, 3, 5, and 7) are disclosed herein. All key positions of cyclin-dependent kinases are conserved in this protein. The regulatory phosphorylation sites at the N-terminus of the molecule found in cdk2 (threonine at position 14 and tyrosine at position 15) are replaced in hPNQALRE by alanine and histidine, respectively, similar to the CDK7-type cyclin-dependent kinases, which also have two residues which cannot be phosphorylated (glutamine and phenylalanine) at these

positions. Regulatory phosphorylation sites of cyclin-dependent kinases are described *inter alia* in Shuttleworth, *Progr. Cell Cycle Res. 1*, 229-40 (1995); Lew & Kornbluth, *Curr. Opin. Cell Biol. 8*, 795-804 (1996); and Morgan, *Ann. Rev. Cell. Biol. 13*, 261-91 (1997). The sequence motif which characterizes the cyclin binding domain of the cyclin-dependent kinases (PSTAIRE in cdk2; SEQ ID NO:15) is replaced in hPNQALRE by the sequence PNQALRE (SEQ ID NO:9), indicating that hPNQALRE has a distinct specificity for its regulatory cyclin subunit.

Various amino acids of hPNQALRE can be substituted to form hPNQALRE variants with one or more altered biological activities. For example the cyclin-dependent kinase activity or cyclin binding domain of hPNQALRE can be altered, or substitutions can be made which permit the protein to be phosphorylated. Such substitutions can provide hPNQALRE with altered regulation or a particular subset of biological activities as compared to wild type hPNQALRE. Cyclin binding domains of other cyclin-dependent kinases, such as PFTAIRE (SEQ ID NO:10), PISSLRE (SEQ ID NO:11), PITALRE (SEQ ID NO:12), PLSTIRE (SEQ ID NO:13), PISTVRE (SEQ ID NO:14), PSTAIRE (SEQ ID NO:15), and NRTALRE (SEQ ID NO:16), can be substituted for the cyclin binding domain of hPNQALRE, PNQALRE (SEQ ID NO:9; amino acids 44-51 of SEQ ID NOS:2 or 4; amino acids 58-64 of SEQ ID NOS:6 and 8) in order to change the cyclin binding specificity of hPNQALRE. Cyclin-dependent kinase activity of hPNQALRE can be modified, for example, by substituting an asparagine for the aspartic acid at position 145; this substitution results in a "kinase-dead" form of hPNQALRE.

Various substitutions can also be made in order to permit hPNQALRE to be phosphorylated. For example, substitution of a phenylalanine or a tyrosine for the histidine at position 15, or substitution of a threonine for the alanine at position 14, permit phosphorylation of hPNQALRE. Other substitutions which affect properties of hPNQALRE will occur to those of skill in the art and can be made to hPNQALRE protein using standard recombinant DNA techniques.

Other amino acid substitutions which do not affect the kinase or cyclin binding activities of hPNQALRE can occur naturally or can be made in the laboratory, to form biologically active hPNQALRE variants. Biologically active variants of hPNQALRE

are involved in cell-cycle regulation, display cyclin-dependent kinase activity, and are over-expressed in tumors. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, such as DNASTAR software.

Preferably, amino acid substitutions in biologically active hPNQALRE variants are conservative amino acid changes, *i.e.*, substitutions of similarly charged or uncharged amino acids. A conservative amino acid change involves substitution of one of a family of amino acids which are related in their side chains. Naturally occurring amino acids are generally divided into four families: acidic (aspartate, glutamate), basic (lysine, arginine, histidine), non-polar (alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), and uncharged polar (glycine, asparagine, glutamine, cystine, serine, threonine, tyrosine) amino acids. Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. It is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid will not have a major effect on the binding properties of the resulting molecule, especially if the replacement does not involve an amino acid at the cyclin-binding site of hPNQALRE or its kinase domain.

Biologically active hPNQALRE variants include glycosylated forms, aggregative conjugates with other molecules, and covalent conjugates with unrelated chemical moieties. Covalent variants can be prepared by linking functionalities to groups which are found in the amino acid chain or at the N- or C-terminal residue, as is known in the art. Biologically active hPNQALRE variants also include allelic variants, species variants, and muteins. Truncations or deletions of regions which do not affect the cyclin-dependent kinase activity of hPNQALRE are also hPNQALRE variants.

Whether an amino acid substitution results in a functional hPNQALRE protein or polypeptide can readily be determined, for example, by assaying its cyclin-dependent kinase activity. Assays for cyclin-dependent kinase activity are taught, for example, in Lock *et al.*, 1997, *Cancer Chemother. Pharmacol. 39*:399-409. Preferred naturally or non-naturally occurring biologically active hPNQALRE variants have amino acid

sequences which are at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to amino acid sequences shown in SEQ ID NOS:2, 4, 6, or 8. More preferably, the molecules are at least 98% or 99% identical. Percent identity can be calculated using any method or algorithm known in the art. A non-limiting example is the Smith-Waterman homology search algorithm, using an affine gap search with the following parameters: a gap open penalty of 12 and a gap extension penalty of 1. The Smith-Waterman homology search algorithm is taught in Smith and Waterman, *Adv. Appl. Math.* (1981) *2*:482-489.

hPNQALRE polypeptides contain less than full-length hPNQALRE and comprise at least 223, 225, 250, 275, 300, or 325 or more contiguous amino acids of an hPNQALRE protein. hPNQALRE polypeptides can comprise the cyclin binding domain of hPNQALRE, PNQALRE (SEQ ID NO:9; amino acids 44-51 of SEQ ID NOS:2 or 4 or amino acids 58-64 of SEQ ID NOS:6 and 8), or can be chimeric polypeptides which comprise hPNQALRE amino acid sequences together with cyclin binding domains of other cyclin-dependent kinases, as disclosed above. Polypeptides in which various amino acid substitutions have been made so as to permit hPNQALRE to be phosphorylated or to decrease kinase activity of hPNQALRE can also be constructed.

hPNQALRE polypeptides of the present invention may comprise amino acids 26-38 of SEQ ID NO:6 or SEQ ID NO:8. Additionally, hPNQALRE polypeptides may comprise amino acids 181-201 of SEQ ID NO:6 or SEQ ID NO:8 or amino acids 168-188 of SEQ ID NO:4.

The present invention contemplates variants of hPNQALRE polypeptides which are at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the polypeptides of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8. For example, the present invention provides hPNQALRE polypeptides that are at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to amino acids 26-38 of SEQ ID NO:6 or SEQ ID NO:8 or that are at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to amino acids 181-201 of SEQ ID NO:6 or SEQ ID NO:8 or amino acids 168-188 of SEQ ID NO:4.

hPNQALRE can be isolated from hPNQALRE-producing human cells, such as spleen, thymus, prostate, testis, small intestine, colon, peripheral blood lymphocytes, heart, brain, placenta, lung, liver, skeletal muscle, kidney, or pancreas, using standard biochemical methods. An isolated and purified hPNQALRE protein or polypeptide is separated from other compounds which normally associate with an hPNQALRE protein or polypeptide in a cell, such as cyclin or other proteins, carbohydrates, lipids, or subcellular organelles. A preparation of isolated and purified hPNQALRE proteins or polypeptides is at least 80% pure; preferably, the preparations are 90%, 95%, or 99% pure.

hPNQALRE proteins and polypeptides can also be produced by recombinant DNA methods or by synthetic chemical methods. For production of recombinant hPNQALRE proteins or polypeptides, coding sequences selected from the *hPNQALRE* nucleotide sequences shown in SEQ ID NOS:1, 3, 5, and 7 or variants of those sequence which encode, for example, an hPNQALRE protein or biologically active or altered hPNQALRE variants, can be expressed in prokaryotic or eukaryotic expression systems. Bacterial, yeast, insect, or mammalian expression systems can be used, as is known in the art. Enzymes can be used to generate hPNQALRE polypeptides by enzymatic proteolysis of full-length hPNQALRE protein.

Alternatively, synthetic chemical methods, such as solid phase peptide synthesis, can be used to synthesize an hPNQALRE protein or polypeptide. General means for the production of peptides, analogs or derivatives are outlined in CHEMISTRY AND BIOCHEMISTRY OF AMINO ACIDS, PEPTIDES, AND PROTEINS -- A SURVEY OF RECENT DEVELOPMENTS, B. Weinstein, ed. (1983). Moreover, substitution of D-amino acids for the normal L-stereoisomer can be carried out to increase the half-life of the molecule. Biologically active hPNQALRE or altered variants can be similarly produced.

Fusion proteins comprising at least 223, 225, 250, 275, 300, or 315 or more contiguous hPNQALRE amino acids can also be constructed. hPNQALRE fusion proteins are useful for generating antibodies which specifically bind to hPNQALRE epitopes and for use in various assay systems. For example, hPNQALRE fusion proteins can be used to identify proteins which interact with hPNQALRE protein, such as different cyclins, and influence its function. Physical methods, such as protein

affinity chromatography, or library-based assays for protein-protein interactions, such as the yeast two-hybrid or phage display systems, can also be used for this purpose. Such methods are well known in the art and can also be used as drug screens.

An hPNQALRE fusion protein comprises two protein segments fused together by means of a peptide bond. The first protein segment can be N-terminal or C-terminal, as is convenient. The first protein segment comprises at least 223, 225, 250, 275, 300, or 315 or more contiguous amino acids of an hPNQALRE protein. The amino acids can be selected from the amino acid sequences shown in SEQ ID NOS:2, 4, 6, and 8 or from a biologically active or altered variant of those sequences. Preferred fusion proteins of the present invention may comprise amino acids 26-38 of SEQ ID NO:6 or SEQ ID NO:8. Also preferred are fusion proteins that comprise amino acids 181-201 of SEQ ID NO:6 or SEQ ID NO:8 or amino acids 168-188 of SEQ ID NO:4. The first protein segment can also comprise a full-length hPNQALRE protein or variant. The first protein segment can be located at the N- or C-terminal of the fusion protein, as is convenient.

The second protein segment can be a full-length protein or a protein fragment or polypeptide. Proteins commonly used in fusion protein construction include β-galactosidase, β-glucoronidase, green fluorescent protein (GFP), autofluorescent proteins, including blue fluorescent protein (BFP), glutathione-S-transferase (GST), luciferase, horseradish peroxidase (HRP), and chloramphenicol acetyltransferase (CAT). Epitope tags can be used in fusion protein constructions, including histidine (His) tags, FLAG tags, influenza hemagglutinin (HA) tags, Myc tags, VSV-G tags, and thioredoxin (Trx) tags. Other fusion constructions can include maltose binding protein (MBP), S-tag, Lex A DNA binding domain (DBD) fusions, GAL4 DNA binding domain fusions, and herpes simplex virus (HSV) BP16 protein fusions.

hPNQALRE fusion proteins can be made by covalently linking the first and second protein segments or by standard procedures in the art of molecular biology. Recombinant DNA methods can be used to prepare hPNQALRE fusion proteins, for example, by making a DNA construct which comprises coding sequences selected from SEQ ID NOS:1, 3, 5, or 7 in proper reading frame with nucleotides encoding the second protein segment and expressing the DNA construct in a host cell, as is known in the art.

Many kits for constructing fusion proteins are available from companies which supply research labs with tools for experiments, including, for example, Promega Corporation (Madison, WI), Stratagene (La Jolla, CA), Clontech (Mountain View, CA), Santa Cruz Biotechnology (Santa Cruz, CA), MBL International Corporation (MIC; Watertown, MA), and Quantum Biotechnologies (Montreal, Canada).

Isolated and purified hPNQALRE proteins, polypeptides, biologically active or altered variants, or fusion proteins can be used as immunogens, to obtain preparations of antibodies which specifically bind to epitopes of an hPNQALRE protein having an amino acid sequence shown in SEQ ID NOS:2, 4, 6, or 8 or a biologically active or altered hPNQALRE variant. Preferably, the antibodies can distinguish between hPNQALRE and other cyclin-dependent kinases, for example by binding to the cyclin-binding site of hPNQALRE. More preferably, antibodies of the present invention will bind to an epitope defined in whole or in part by amino acids 26-38 of SEQ ID NO:6 or SEQ ID NO:8. Also preferred are antibodies that bind to an epitope defined in whole or in part by amino acids 181-201 of SEQ ID NO:6 or SEQ ID NO:8 or amino acids 168-188 of SEQ ID NO:4. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an hPNQALRE epitope. However, epitopes which involve non-contiguous amino acids may require more, *e.g.*, at least 15, 25, or 50 amino acids.

Antibodies which specifically bind to epitopes of hPNQALRE proteins, polypeptides, fusion proteins, or biologically active variants can be used in immunochemical assays, including but not limited to Western blots, ELISAs, radioimmunoassays, immunohistochemical assays, immunoprecipitations, or other immunochemical assays known in the art. Typically, antibodies of the invention provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in such immunochemical assays. Preferably, antibodies which specifically bind to hPNQALRE epitopes do not detect other proteins in immunochemical assays and can immunoprecipitate hPNQALRE protein or polypeptides from solution.

Epitopes of hPNQALRE which are particularly antigenic can be selected, for example, by routine screening of hPNQALRE polypeptides for antigenicity or by applying a theoretical method for selecting antigenic regions of a protein to the amino

acid sequences shown in SEQ ID NOS:2, 4, 6, or 8. Such methods are taught, for example, in Hopp and Wood, *Proc. Natl. Acad. Sci. U.S.A. 78*, 3824-28 (1981), Hopp and Wood, *Mol. Immunol. 20*, 483-89 (1983), and Sutcliffe *et al.*, *Science 219*, 660-66 (1983).

Any type of antibody known in the art can be generated to bind specifically to hPNQALRE epitopes. For example, preparations of polyclonal and monoclonal antibodies can be made using standard methods which are well known in the art. Similarly, single-chain antibodies can also be prepared. Single-chain antibodies which specifically bind to hPNQALRE epitopes can be isolated, for example, from single-chain immunoglobulin display libraries, as is known in the art. The library is "panned" against hPNQALRE amino acid sequences, and a number of single chain antibodies which bind with high-affinity to different epitopes of hPNQALRE protein can be isolated. Hayashi *et al.*, 1995, *Gene 160*:129-30. Single-chain antibodies can also be constructed using a DNA amplification method, such as the polymerase chain reaction (PCR), using hybridoma cDNA as a template. Thirion *et al.*, 1996, *Eur. J. Cancer Prev. 5*:507-11.

Single-chain antibodies can be mono- or bispecific, and can be bivalent or tetravalent. Construction of tetravalent, bispecific single-chain antibodies is taught, for example, in Coloma and Morrison, 1997, *Nat. Biotechnol. 15*:159-63. Construction of bivalent, bispecific single-chain antibodies is taught *inter alia* in Mallender and Voss, 1994, *J. Biol. Chem. 269*:199-206.

A nucleotide sequence encoding a single-chain antibody can be constructed using manual or automated nucleotide synthesis, cloned into an expression construct using standard recombinant DNA methods, and introduced into a cell to express the coding sequence, as described below. Alternatively, single-chain antibodies can be produced directly using, for example, filamentous phage technology. Verhaar *et al.*, 1995, *Int. J. Cancer 61*:497-501; Nicholls *et al.*, 1993, *J. Immunol. Meth. 165*:81-91.

Monoclonal and other antibodies can also be "humanized" in order to prevent a patient from mounting an immune response against the antibody when it is used therapeutically. Such antibodies may be sufficiently similar in sequence to human antibodies to be used directly in therapy or may require alteration of a few key residues.

Sequence differences between, for example, rodent antibodies and human sequences can be minimized by replacing residues which differ from those in the human sequences, for example, by site directed mutagenesis of individual residues, or by grafting of entire complementarity determining regions. Alternatively, one can produce humanized antibodies using recombinant methods, as described in GB2188638B. Antibodies which specifically bind to hPNQALRE epitopes can contain antigen binding sites which are either partially or fully humanized, as disclosed in U.S. 5,565,332.

Other types of antibodies can be constructed and used in methods of the invention. For example, chimeric antibodies can be constructed as disclosed, for example, in WO 93/03151. Binding proteins which are derived from immunoglobulins and which are multivalent and multispecific, such as the "diabodies" described in WO 94/13804, can also be prepared.

Antibodies of the invention can be purified by methods well known in the art. For example, antibodies can be affinity purified by passing the antibodies over a column to which an hPNQALRE protein, polypeptide, biologically active variant, or fusion protein is bound. The bound antibodies can then be eluted from the column, using a buffer with a high salt concentration.

hPNQALRE-specific binding polypeptides other than antibodies can also be generated. hPNQALRE-specific binding polypeptides are polypeptides which bind with hPNQALRE or its variants and which have a measurably higher binding affinity for hPNQALRE and polypeptide derivatives of hPNQALRE than for other polypeptides tested for binding. Higher affinity by a factor of 10 is preferred, more preferably a factor of 100. Such polypeptides can be found, for example, using the yeast two-hybrid system.

Antibodies can be used, *inter alia*, to detect wild-type hPNQALRE protein in human tissue and fractions thereof. The antibodies can also be used to detect the presence of mutations in the *hPNQALRE* gene which result in under- or over-expression of an hPNQALRE protein or in expression of an hPNQALRE protein with altered size or electrophoretic mobility. Optionally, antibodies of the invention can be used to block hPNQALRE cyclin binding sites or to alter effective levels of functional hPNQALRE protein. Alternatively, Antibodies may be used to detect polypeptides comprising

amino acids 26-38 of SEQ ID NO:6 or SEQ ID NO:8. Preferred antibodies will bind to and block the biological activity defined by the T-loop region which includes amino acids 181-201 of SEQ ID NO:6 or SEQ ID NO:8 or amino acids 168-188 of SEQ ID NO:4.

The invention also provides subgenomic polynucleotides which encodes hPNQALRE proteins, polypeptides, biologically active or altered variants, fusion proteins, and the like. *hPNQALRE* subgenomic polynucleotides contain less than a whole chromosome and can be double- or single-stranded. Preferably, the polynucleotides are intron-free.

hPNQALRE subgenomic polynucleotides can comprise at least 1562, 1563, 1670, 1575, 1800, 1859, 1900, 1950, 2000, 2050, or 2100 or more contiguous nucleotides selected from the nucleotide sequences shown in SEQ ID NOS:1, 3, 5, or 7 or their complements. Complementary nucleotide sequences can be used provide *hPNQALRE* antisense oligonucleotides. Preferred antisense oligonucleotides that are encompassed by nucleotides 76-114 of SEQ ID NO:5 or SEQ ID NO:7. Also preferred are antisense oligonucleotides that are encompassed by nucleotides 503-564 of SEQ ID NO:3, nucleotides 542-603 of SEQ ID NO:5 or SEQ ID NO:7. *hPNQALRE* subgenomic polynucleotides also include polynucleotides which encode hPNQALRE-specific single-chain antibodies, ribozymes, and biologically active or altered hPNQALRE variants.

Degenerate nucleotide sequences encoding amino acid sequences of hPNQALRE protein or biologically active hPNQALRE variants, as well as homologous nucleotide sequences which are at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleotide sequences shown in SEQ ID NOS:1, 3, 5, or 7 are also *hPNQALRE* subgenomic polynucleotides. Preferred subgenomic polynucleotides include nucleotides which are at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to 76-114 of SEQ ID NO:5 or SEQ ID NO:7 as well as nucleotides 503-564 of SEQ ID NO:3 and nucleotides 542-603 of SEQ ID NO:5 or SEQ ID NO:7. Percent sequence identity may be determined using computer programs which employ the Smith-Waterman algorithm, for example as implemented in the MPSRCH program

(Oxford Molecular), using an affine gap search with the following parameters: a gap open penalty of 12 and a gap extension penalty of 1.

Nucleotide sequences which hybridize to the coding sequences shown in SEQ ID NOS:1, 3, 5, and 7 or their complements with at most 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, or 35% basepair mismatches are also *hPNQALRE* subgenomic polynucleotides of the invention. Preferred nucleotide sequences will hybridize with at most 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, or 35% basepair mismatches to nucleotides 76-114 of SEQ ID NO:5 or SEQ ID NO:7 as well as nucleotides 503-564 of SEQ ID NO:3 and nucleotides 542-603 of SEQ ID NO:5 or SEQ ID NO:7. For example, using the following wash conditions--2X SSC (0.3 M sodium chloride, 0.03 M sodium citrate, pH 7.0), 0.1% SDS, room temperature twice, 30 minutes each; then 2X SSC, 0.1% SDS, 50 °C once, 30 minutes; then 2X SSC, room temperature twice, 10 minutes each--homologous *hPNQALRE* sequences can be identified which contain at most about 25-30% basepair mismatches with SEQ ID NOS:1, 3, 5, or 7 or their complements. More preferably, homologous nucleic acid strands contain 15-25% basepair mismatches, even more preferably 5-15% basepair mismatches.

Species homologs of *hPNQALRE* subgenomic polynucleotides of the invention can also be identified by making suitable probes or primers and screening cDNA expression libraries from other species, such as mice, monkeys, yeast, or bacteria. It is well known that the T_m of a double-stranded DNA decreases by 1-1.5 °C with every 1% decrease in homology (Bonner *et al.*, *J. Mol. Biol. 81*, 123 (1973). Homologous *hPNQALRE* polynucleotides can therefore be identified, for example, by hybridizing a putative homologous *hPNQALRE* polynucleotide with a polynucleotide having the nucleotide sequence of SEQ ID NOS:1, 3, 5, or 7, comparing the melting temperature of the test hybrid with the melting temperature of a hybrid comprising a polynucleotide having SEQ ID NOS:1, 3, 5, or 7 and a polynucleotide which is perfectly complementaryto that sequence, and calculating the number or percent of basepair mismatches within the test hybrid.

Nucleotide sequences which hybridize to the coding sequences shown in SEQ ID NOS:1, 3, 5, or 7 or their complements following stringent hybridization and/or wash conditions are also *hPNQALRE* subgenomic polynucleotides of the invention.

Stringent wash conditions are well known and understood in the art and are disclosed, for example, in Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL, 2d ed., 1989, at pages 9.50-9.51. Preferred species homologs of hPNQALRE subgenomic polynucleotides will hybridize under stringent conditions to nucleotides 76-114 of SEQ ID NO:5 or SEQ ID NO:7 or to nucleotides 503-564 of SEQ ID NO:3 and nucleotides 542-603 of SEQ ID NO:5 or SEQ ID NO:7.

Typically, for stringent hybridization conditions, a combination of temperature and salt concentration should be chosen that is approximately 12-20 °C below the calculated T_m of the hybrid under study. The T_m of a hybrid between the *hPNQALRE* sequence shown in SEQ ID NOS:1, 3, 5, or 7 and a polynucleotide sequence which is 65%, 75%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical can be calculated, for example, using the equation of Bolton and McCarthy, *Proc. Natl. Acad. Sci. U.S.A. 48*, 1390 (1962):

$$T_m = 81.5\ ^{\circ}C - 16.6(\log_{10}[Na^+]) + 0.41(\%G + C) - 0.63(\%\text{formamide}) - 600/l),$$

where l = the length of the hybrid in basepairs.

Stringent wash conditions include, for example, 4X SSC at 65 °C, or 50% formamide, 4X SSC at 42 °C, or 0.5X SSC, 0.1% SDS at 65 °C. Highly stringent wash conditions include, for example, 0.2X SSC at 65 °C.

hPNQALRE subgenomic polynucleotides can be isolated and purified free from other nucleotide sequences using standard nucleic acid purification techniques. For example, restriction enzymes and probes can be used to isolate polynucleotide fragments which comprise nucleotide sequences encoding an hPNQALRE protein or variant. Isolated and purified subgenomic polynucleotides are in preparations which are free or at least 90% free of other molecules.

Complementary DNA (cDNA) molecules which encode hPNQALRE proteins are also *hPNQALRE* subgenomic polynucleotides of the invention. *hPNQALRE* cDNA molecules can be made with standard molecular biology techniques, using *hPNQALRE* mRNA as a template. *hPNQALRE* cDNA molecules can thereafter be replicated using molecular biology techniques known in the art and disclosed in manuals such as Sambrook *et al.*, 1989. An amplification technique, such as the polymerase chain

reaction (PCR), can be used to obtain additional copies of subgenomic polynucleotides of the invention, using either human genomic DNA or cDNA as a template.

Alternatively, synthetic chemistry techniques can be used to synthesize *hPNQALRE* subgenomic polynucleotide molecules of the invention. The degeneracy of the genetic code allows alternate nucleotide sequences to be synthesized which will encode an hPNQALRE protein having the amino acid sequences shown in SEQ ID NOS:2, 4, 6, or 8 or a biologically active variant of those sequences. All such nucleotide sequences are within the scope of the present invention.

The invention also provides polynucleotide probes which can be used to detect *hPNQALRE* sequences, for example, in hybridization protocols such as Northern or Southern blotting or *in situ* hybridization. Polynucleotide probes of the invention comprise at least 12, 13, 14, 15, 16, 17, 18, 19, 20, 30, or 40 or more contiguous nucleotides selected from SEQ ID NOS:1, 3, 5, or 7. Preferred probes comprise at least 12, 13, 14, 15, 16, 17, 18, 19, 20, 30, or 40 or more contiguous nucleotides selected from nucleotides 76-114 of SEQ ID NO:5 or SEQ ID NO:7 or nucleotides 503-564 of SEQ ID NO:3 and nucleotides 542-603 of SEQ ID NO:5 or SEQ ID NO:7. Polynucleotide probes of the invention can comprise a detectable label, such as a radioisotopic, fluorescent, enzymatic, or chemiluminescent label.

An *hPNQALRE* construct can be an expression construct which comprises a promoter which is functional in a selected host cell. The skilled artisan can readily select an appropriate promoter from the large number of cell type-specific promoters known and used in the art. The expression construct can also contain a transcription terminator which is functional in the host cell. The expression construct comprises a polynucleotide segment which encodes, for example, all or a portion of an hPNQALRE protein, variant, fusion protein, antibody, or ribozyme. The polynucleotide segment is located downstream from the promoter. Transcription of the polynucleotide segment initiates at the promoter.

A recombinant host cell comprising an *hPNQALRE* construct can be constructed, for example, to express all or a portion of an hPNQALRE protein. Preferred host cells express a portion of an hPNQALRE protein that comprises amino acids 26-38 of SEQ ID NO:6 or SEQ ID NO:8. Also preferred are host cells that

express a portion of an hPNQALRE protein that comprises amino acids 181-201 of SEQ ID NO:6 or SEQ ID NO:8 as well as amino acids 168-188 of SEQ ID NO:4. Recombinant host cells comprising *hPNQALRE* expression constructs can be prokaryotic or eukaryotic. A variety of host cells are available for use in bacterial, yeast, insect, and human expression systems and can be used to express or to propagate *hPNQALRE* expression constructs.

Constructs can be introduced into host cells using any technique known in the art. These techniques include transferrin-polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated cellular fusion, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, and calcium phosphate-mediated transfection.

Bacterial systems for expressing *hPNQALRE* expression constructs include those described in Chang *et al., Nature* (1978) *275*: 615, Goeddel *et al., Nature* (1979) *281*: 544, Goeddel *et al., Nucleic Acids Res.* (1980) *8*: 4057, EP 36,776, U.S. 4,551,433, deBoer *et al., Proc. Natl. Acad. Sci. USA* (1983) *80*: 21-25, and Siebenlist *et al., Cell* (1980) *20*: 269.

Expression systems in yeast include those described in Hinnen *et al., Proc. Natl. Acad. Sci. USA* (1978) *75*: 1929; Ito *et al., J. Bacteriol.* (1983) *153*: 163; Kurtz *et al., Mol. Cell. Biol.* (1986) *6*: 142; Kunze *et al., J. Basic Microbiol.* (1985) *25*: 141; Gleeson *et al., J. Gen. Microbiol.* (1986) *132*: 3459, Roggenkamp *et al., Mol. Gen. Genet.* (1986) *202* :302) Das *et al., J. Bacteriol.* (1984) *158*: 1165; De Louvencourt *et al., J. Bacteriol.* (1983) *154*: 737, Van den Berg *et al., Bio/Technology* (1990) *8*: 135; Kunze *et al., J. Basic Microbiol.* (1985) *25*: 141; Cregg *et al., Mol. Cell. Biol.* (1985) *5*: 3376, U.S. 4,837,148, US 4,929,555; Beach and Nurse, *Nature* (1981) *300*: 706; Davidow *et al., Curr. Genet.* (1985) *10*: 380, Gaillardin *et al., Curr. Genet.* (1985) *10*: 49, Ballance *et al., Biochem. Biophys. Res. Commun.* (1983) *112*: 284-289; Tilburn *et al., Gene* (1983) *26*: 205-221, Yelton *et al., Proc. Natl. Acad. Sci. USA* (1984) *81*: 1470-1474, Kelly and Hynes, *EMBO J.* (1985) *4*: 475479; EP 244,234, and WO 91/00357.

Expression of *hPNQALRE* expression constructs in insects can be carried out as described in U.S. 4,745,051, Friesen *et al.* (1986) "The Regulation of Baculovirus Gene

Expression" in: THE MOLECULAR BIOLOGY OF BACULOVIRUSES (W. Doerfler, ed.), EP 127,839, EP 155,476, and Vlak *et al., J. Gen. Virol.* (1988) *69*: 765-776, Miller *et al., Ann. Rev. Microbiol.* (1988) *42*: 177, Carbonell *et al., Gene* (1988) *73*: 409, Maeda *et al., Nature* (1985) *315*: 592-594, Lebacq-Verheyden *et al., Mol. Cell. Biol.* (1988) *8*: 3129; Smith *et al., Proc. Natl. Acad. Sci. USA* (1985) *82*: 8404, Miyajima *et al., Gene* (1987) *58*: 273; and Martin *et al., DNA* (1988) *7*:99. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts are described in Luckow *et al., Bio/Technology* (1988) *6:* 47-55, Miller *et al.,* in GENETIC ENGINEERING (Setlow, J.K. *et al.* eds.), Vol. 8 (Plenum Publishing, 1986), pp. 277-279, and Maeda *et al., Nature,* (1985) *315*: 592-594.

Mammalian expression of *hPNQALRE* expression constructs can be achieved as described in Dijkema *et al., EMBO J.* (1985) *4*: 761, Gorman *et al., Proc. Natl. Acad. Sci. USA* (1982b) *79*: 6777, Boshart *et al., Cell* (1985) *41*: 521 and U.S. 4,399,216. Other features of mammalian expression of *hPNQALRE* expression constructs can be facilitated as described in Ham and Wallace, *Meth. Enz.* (1979) *58*: 44, Barnes and Sato, *Anal. Biochem.* (1980) *102*: 255, U.S. 4,767,704, US 4,657,866, US 4,927,762, US 4,560,655, WO 90/103430, WO 87/00195, and U.S. RE 30,985.

Subgenomic polynucleotides of the invention can also be used in gene delivery vehicles, for the purpose of delivering an *hPNQALRE* mRNA or oligonucleotide (either with the sequence of native *hPNQALRE* mRNA or its complement), full-length hPNQALRE protein, hPNQALRE fusion protein, hPNQALRE polypeptide, biologically active or altered variant, or hPNQALRE-specific ribozyme or single-chain antibody into a cell, preferably a eukaryotic cell. According to the present invention, a gene delivery vehicle can be, for example, naked plasmid DNA, a viral expression vector comprising an *hPNQALRE* subgenomic polynucleotide, or an *hPNQALRE* subgenomic polynucleotide in conjunction with a liposome or a condensing agent.

In one embodiment of the invention, the gene delivery vehicle comprises a promoter and an *hPNQALRE* subgenomic polynucleotide. Preferred promoters are tissue-specific promoters and promoters which are activated by cellular proliferation, such as the thymidine kinase and thymidylate synthase promoters. Other preferred promoters include promoters which are activatable by infection with a virus, such as the

α- and β-interferon promoters, and promoters which are activatable by a hormone, such as estrogen. Other promoters which can be used include the Moloney virus LTR, the CMV promoter, and the mouse albumin promoter.

An *hPNQALRE* gene delivery vehicle can comprise viral sequences such as a viral origin of replication or packaging signal. These viral sequences can be selected from viruses such as astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, retrovirus, togavirus or adenovirus. In a preferred embodiment, the *hPNQALRE* gene delivery vehicle is a recombinant retroviral vector. Recombinant retroviruses and various uses thereof have been described in numerous references including, for example, Mann *et al.*, *Cell 33:*153, 1983, Cane and Mulligan, *Proc. Nat'l. Acad. Sci. USA 81*:6349, 1984, Miller *et al.*, *Human Gene Therapy* 1:5-14, 1990, U.S. Patent Nos. 4,405,712, 4,861,719, and 4,980,289, and PCT Application Nos. WO 89/02,468, WO 89/05,349, and WO 90/02,806.

Numerous retroviral gene delivery vehicles can be utilized in the present invention, including for example those described in EP 0,415,731; WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; U.S. Patent No. 5,219,740; WO 9311230; WO 9310218; Vile and Hart, *Cancer Res. 53*:3860-3864, 1993; Vile and Hart, *Cancer Res. 53*:962-967, 1993; Ram *et al.*, *Cancer Res. 53*:83-88, 1993; Takamiya *et al.*, *J. Neurosci. Res. 33*:493-503, 1992; Baba *et al.*, *J. Neurosurg. 79*:729-735, 1993 (U.S. Patent No. 4,777,127, GB 2,200,651, EP 0,345,242 and WO91/02805).

Particularly preferred retroviruses are derived from retroviruses which include avian leukosis virus (ATCC Nos. VR-535 and VR-247), bovine leukemia virus (VR-1315), murine leukemia virus (MLV), mink-cell focus-inducing virus (Koch *et al.*, *J. Vir. 49*:828, 1984; and Oliff *et al.*, *J. Vir. 48*:542, 1983), murine sarcoma virus (ATCC Nos. VR-844, 45010 and 45016), reticuloendotheliosis virus (ATCC Nos VR-994, VR-770 and 45011), Rous sarcoma virus, Mason-Pfizer monkey virus, baboon endogenous virus, endogenous feline retrovirus (*e.g.*, RD114), and mouse or rat gL30 sequences used as a retroviral vector.

Particularly preferred strains of MLV from which recombinant retroviruses can be generated include 4070A and 1504A (Hartley and Rowe, *J. Vir. 19*:19, 1976),

Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi (Ru *et al.*, *J. Vir.* *67*:4722, 1993; and Yantchev *Neoplasma 26*:397, 1979), Gross (ATCC No. VR-590), Kirsten (Albino *et al.*, *J. Exp. Med. 164*:1710, 1986), Harvey sarcoma virus (Manly *et al.*, *J. Vir. 62*:3540, 1988; and Albino *et al.*, *J. Exp. Med. 164*:1710, 1986) and Rauscher (ATCC No. VR-998), and Moloney MLV (ATCC No. VR-190).

A particularly preferred non-mouse retrovirus is Rous sarcoma virus. Preferred Rous sarcoma viruses include Bratislava (Manly *et al.*, *J. Vir. 62*:3540, 1988; and Albino *et al.*, *J. Exp. Med. 164*:1710, 1986), Bryan high titer (*e.g.*, ATCC Nos. VR-334, VR-657, VR-726, VR-659, and VR-728), Bryan standard (ATCC No. VR-140), Carr-Zilber (Adgighitov *et al.*, *Neoplasma 27*:159, 1980), Engelbreth-Holm (Laurent *et al.*, *Biochem Biophys Acta* 908:241, 1987), Harris, Prague (*e.g.*, ATCC Nos. VR-772, and 45033), and Schmidt-Ruppin (*e.g.* ATCC Nos. VR-724, VR-725, VR-354) viruses.

Any of the above retroviruses can be readily utilized in order to assemble or construct retroviral *hPNQALRE* gene delivery vehicles given the disclosure provided herein and standard recombinant techniques (*e.g.*, Sambrook *et al., Molecular Cloning: A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory Press, 1989, and Kunkle, *PNAS 82*:488, 1985) known in the art. Portions of retroviral *hPNQALRE* expression vectors can be derived from different retroviruses. For example, retrovector LTRs can be derived from a murine sarcoma virus, a tRNA binding site from a Rous sarcoma virus, a packaging signal from a murine leukemia virus, and an origin of second strand synthesis from an avian leukosis virus.

Recombinant retroviral vectors can be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (*see* Serial No. 07/800,921, filed November 29, 1991). Recombinant retroviruses can be produced which direct the site-specific integration of the recombinant retroviral genome into specific regions of the host cell DNA. Site-specific integration can be mediated by a chimeric integrase incorporated into the retroviral particle (*see* Serial No. 08/445,466 filed May 22, 1995). It is preferable that the recombinant viral gene delivery vehicle is a replication-defective recombinant virus.

Packaging cell lines suitable for use with the above-described retroviral gene delivery vehicles can be readily prepared (*see* Serial No. 08/240,030, filed May 9, 1994;

see also WO 92/05266) and used to create producer cell lines (also termed vector cell lines or "VCLs") for production of recombinant viral particles. In particularly preferred embodiments of the present invention, packaging cell lines are made from human (*e.g.*, HT1080 cells) or mink parent cell lines, thereby allowing production of recombinant retroviral gene delivery vehicles which are capable of surviving inactivation in human serum. The construction of recombinant retroviral gene delivery vehicles is described in detail in WO 91/02805.

Recombinant retroviral gene delivery vehicles can be used to generate transduction competent retroviral particles by introducing them into appropriate packaging cell lines (*see* Serial No. 07/800,921). Similarly, adenovirus gene delivery vehicles can also be readily prepared and utilized given the disclosure provided herein (*see also* Berkner, *Biotechniques 6*:616-627, 1988, and Rosenfeld *et al.*, *Science 252*:431-434, 1991, WO 93/07283, WO 93/06223, and WO 93/07282).

An *hPNQALRE* gene delivery vehicle can also be a recombinant adenoviral gene delivery vehicle. Such vehicles can be readily prepared and utilized given the disclosure provided herein (*see* Berkner, *Biotechniques 6*:616, 1988, and Rosenfeld *et al.*, *Science 252*:431, 1991, WO 93/07283, WO 93/06223, and WO 93/07282). Adeno-associated viral *hPNQALRE* gene delivery vehicles can also be constructed and used to deliver hPNQALRE amino acids or nucleotides.

The use of adeno-associated viral gene delivery vehicles *in vitro* is described in Chatterjee *et al.*, *Science 258*: 1485-1488 (1992), Walsh *et al.*, *Proc. Nat'l. Acad. Sci. 89*: 7257-7261 (1992), Walsh *et al.*, *J. Clin. Invest. 94*: 1440-1448 (1994), Flotte *et al.*, *J. Biol. Chem. 268*: 3781-3790 (1993), Ponnazhagan *et al.*, *J. Exp. Med. 179*: 733-738 (1994), Miller *et al.*, *Proc. Nat'l Acad. Sci. 91:* 10183-10187 (1994), Einerhand *et al.*, *Gene Ther. 2*: 336-343 (1995), Luo *et al.*, *Exp. Hematol. 23*: 1261-1267 (1995), and Zhou *et al.*, *Gene Therapy 3:* 223-229 (1996). *In vivo* use of these vehicles is described in Flotte *et al.*, *Proc. Nat'l Acad. Sci. 90*: 10613-10617 (1993), and Kaplitt *et al.*, *Nature Genet. 8*:148-153 (1994).

In another embodiment of the invention, an *hPNQALRE* gene delivery vehicle is derived from a togavirus. Preferred togaviruses include alphaviruses, in particular those described in U.S. Serial No. 08/405,627, filed March 15, 1995, WO 95/07994. Alpha

viruses, including Sindbis and ELVS viruses can be gene delivery vehicles for *hPNQALRE* polynucleotides. Alpha viruses are described in WO 94/21792, WO 92/10578 and WO 95/07994. Several different alphavirus gene delivery vehicle systems can be constructed and used to deliver *hPNQALRE* subgenomic polynucleotides to a cell according to the present invention. Representative examples of such systems include those described in U.S. Patents 5,091,309 and 5,217,879. Particularly preferred alphavirus gene delivery vehicles for use in the present invention include those which are described in WO 95/07994, and U.S. Serial No. 08/405,627.

Preferably, the recombinant viral vehicle is a recombinant alphavirus viral vehicle based on a Sindbis virus. Sindbis constructs, as well as numerous similar constructs, can be readily prepared essentially as described in U.S. Serial No. 08/198,450. Sindbis viral gene delivery vehicles typically comprise a 5' sequence capable of initiating Sindbis virus transcription, a nucleotide sequence encoding Sindbis non-structural proteins, a viral junction region inactivated so as to prevent subgenomic fragment transcription, and a Sindbis RNA polymerase recognition sequence. Optionally, the viral junction region can be modified so that subgenomic polynucleotide transcription is reduced, increased, or maintained. As will be appreciated by those in the art, corresponding regions from other alphaviruses can be used in place of those described above.

The viral junction region of an alphavirus-derived gene delivery vehicle can comprise a first viral junction region which has been inactivated in order to prevent transcription of the subgenomic polynucleotide and a second viral junction region which has been modified such that subgenomic polynucleotide transcription is reduced. An alphavirus-derived vehicle can also include a 5' promoter capable of initiating synthesis of viral RNA from cDNA and a 3' sequence which controls transcription termination.

Other recombinant togaviral gene delivery vehicles which can be utilized in the present invention include those derived from Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in U.S. Patents 5,091,309 and 5,217,879 and in WO 92/10578. The Sindbis vehicles described above,

as well as numerous similar constructs, can be readily prepared essentially as described in U.S. Serial No. 08/198,450.

Other viral gene delivery vehicles suitable for use in the present invention include, for example, those derived from poliovirus (Evans *et al.*, *Nature 339*:385, 1989, and Sabin *et al.*, *J. Biol. Standardization 1*:115, 1973) (ATCC VR-58); rhinovirus (Arnold *et al.*, *J. Cell. Biochem.* L401, 1990) (ATCC VR-1110); pox viruses, such as canary pox virus or vaccinia virus (Fisher-Hoch *et al.*, *PNAS 86*:317, 1989; Flexner *et al.*, *Ann. N.Y. Acad. Sci. 569*:86, 1989; Flexner *et al.*, *Vaccine 8*:17, 1990; U.S. 4,603,112 and U.S. 4,769,330; WO 89/01973) (ATCC VR-111; ATCC VR-2010); SV40 (Mulligan *et al.*, *Nature 277:*108, 1979) (ATCC VR-305), (Madzak *et al.*, *J. Gen. Vir. 73*:1533, 1992); and influenza virus (Luytjes *et al.*, *Cell 59*:1107, 1989; McMicheal *et al.*, *The New England Journal of Medicine 309*:13, 1983; and Yap *et al.*, *Nature 273*:238, 1978) (ATCC VR-797).

Other viruses which can be used to derive gene delivery vehicles include parvoviruses such as adeno-associated virus (Samulski *et al.*, *J. Vir. 63*:3822, 1989, and Mendelson *et al.*, *Virology 166*:154, 1988) (ATCC VR-645); herpes simplex virus (Kit *et al.*, *Adv. Exp. Med. Biol. 215*:219, 1989) (ATCC VR-977; ATCC VR-260); *Nature 277*: 108, 1979); human immunodeficiency virus (EPO 386,882, Buchschacher *et al.*, *J. Vir. 66*:2731, 1992); and measles virus (EPO 440,219) (ATCC VR-24); A (ATCC VR-67; ATCC VR-1247).

Aura (ATCC VR-368), Bebaru virus (ATCC VR-600; ATCC VR-1240), Cabassou (ATCC VR-922), Chikungunya virus (ATCC VR-64; ATCC VR-1241), Fort Morgan (ATCC VR-924), Getah virus (ATCC VR-369; ATCC VR-1243), Kyzylagach (ATCC VR-927), Mayaro (ATCC VR-66), Mucambo virus (ATCC VR-580; ATCC VR-1244), Ndumu (ATCC VR-371), Pixuna virus (ATCC VR-372; ATCC VR-1245), Tonate (ATCC VR-925), Triniti (ATCC VR-469), Una (ATCC VR-374), Whataroa (ATCC VR-926), Y-62-33 (ATCC VR-375), O'Nyong virus, Eastern encephalitis virus (ATCC VR-65; ATCC VR-1242), Western encephalitis virus (ATCC VR-70; ATCC VR-1251; ATCC VR-622; ATCC VR-1252), and coronavirus (Hamre *et al.*, *Proc. Soc. Exp. Biol. Med. 121*:190, 1966) (ATCC VR-740) can also be used to provide gene delivery vehicles.

An *hPNQALRE* subgenomic polynucleotide of the invention can be combined with a condensing agent to form a gene delivery vehicle. In a preferred embodiment, the condensing agent is a polycation, such as polylysine, polyarginine, polyornithine, protamine, spermine, spermidine, and putrescine. Many suitable methods for making such linkages are known in the art (see, for example, Serial No. 08/366,787, filed December 30, 1994).

Alternatively, an *hPNQALRE* subgenomic polynucleotide can be with a liposome to form a gene delivery vehicle. Liposomes are small, lipid vesicles comprised of an aqueous compartment enclosed by a lipid bilayer, typically spherical or slightly elongated structures several hundred Angstroms in diameter. Under appropriate conditions, a liposome can fuse with the plasma membrane of a cell or with the membrane of an endocytic vesicle within a cell which has internalized the liposome, thereby releasing its contents into the cytoplasm. Prior to interaction with the surface of a cell, however, the liposome membrane acts as a relatively impermeable barrier which sequesters and protects its contents, for example, from degradative enzymes.

Additionally, because a liposome is a synthetic structure, specially designed liposomes can be produced which incorporate desirable features. *See* Stryer, *Biochemistry*, pp. 236-240, 1975 (W.H. Freeman, San Francisco, CA); Szoka *et al.*, *Biochim. Biophys. Acta 600*:1, 1980; Bayer *et al.*, *Biochim. Biophys. Acta. 550*:464, 1979; Rivnay *et al.*, *Meth. Enzymol. 149*:119, 1987; Wang *et al.*, *PNAS 84*: 7851, 1987, Plant *et al.*, *Anal. Biochem. 176*:420, 1989, and U.S. Patent 4,762,915. Liposomes can encapsulate a variety of nucleic acid molecules including DNA, RNA, plasmids, and expression constructs comprising *hPNQALRE* subgenomic polynucleotides such those disclosed in the present invention.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner *et al.*, *Proc. Natl. Acad. Sci. USA 84*:7413-7416, 1987), mRNA (Malone *et al.*, *Proc. Natl. Acad. Sci. USA 86*:6077-6081, 1989), and purified transcription factors (Debs *et al.*, *J. Biol. Chem. 265*:10189-10192, 1990), in functional form. Cationic liposomes are readily available. For example, N[1-2,3-dioleyloxy)propyl]-N,N,N-triethylammonium

(DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. *See also* Felgner *et al.*, *Proc. Natl. Acad. Sci. USA 91:* 5148-5152.87, 1994.

Other commercially available liposomes include Transfectace (DDAB/DOPE) and DOTAP/DOPE (Boerhinger). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. *See, e.g.*, Szoka *et al.*, *Proc. Natl. Acad. Sci. USA 75*:4194-4198, 1978; and WO 90/11092 for descriptions of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphoshatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilammelar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. *See, e.g.,* Straubinger *et al.*, METHODS OF IMMUNOLOGY (1983), Vol. 101, pp. 512-527; Szoka *et al.*, *Proc. Natl. Acad. Sci. USA 87*:3410-3414, 1990; Papahadjopoulos *et al.*, *Biochim. Biophys. Acta 394*:483, 1975; Wilson *et al.*, *Cell 17*:77, 1979; Deamer and Bangham, *Biochim. Biophys. Acta 443*:629, 1976; Ostro *et al.*, *Biochem. Biophys. Res. Commun. 76*:836 , 1977; Fraley *et al.*, *Proc. Natl. Acad. Sci. USA 76*:3348, 1979; Enoch and Strittmatter, *Proc. Natl. Acad. Sci. USA 76*:145, 1979; Fraley *et al.*, *J. Biol. Chem. 255*:10431, 1980; Szoka and Papahadjopoulos, *Proc. Natl. Acad. Sci. USA 75*:145, 1979; and Schaefer-Ridder *et al.*, *Science 215*:166, 1982.

In addition, lipoproteins can be included with an *hPNQALRE* subgenomic polynucleotide for delivery to a cell. Examples of such lipoproteins include chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Modifications of naturally occurring lipoproteins can also be

used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are included with a polynucleotide, no other targeting ligand is included in the composition.

"Naked" *hPNQALRE* subgenomic polynucleotide molecules can also be used as gene delivery vehicles, as described in WO 90/11092 and U.S. Patent 5,580,859. Such gene delivery vehicles can be either *hPNQALRE* DNA or RNA and, in certain embodiments, are linked to killed adenovirus. Curiel *et al.*, *Hum. Gene. Ther.* *3*:147-154, 1992. Other suitable vehicles include DNA-ligand (Wu *et al.*, *J. Biol. Chem.* *264*:16985-16987, 1989), lipid-DNA combinations (Felgner *et al.*, *Proc. Natl. Acad. Sci. USA* *84*:7413 7417, 1989), liposomes (Wang *et al.*, *Proc. Natl. Acad. Sci.* *84*:7851-7855, 1987) and microprojectiles (Williams *et al.*, *Proc. Natl. Acad. Sci.* *88*:2726-2730, 1991).

The efficiency of naked *hPNQALRE* subgenomic polynucleotide uptake into cells can be increased by coating the polynucleotides onto biodegradable latex beads, which are efficiently transported and concentrated in the perinuclear region of the cells. *hPNQALRE* subgenomic polynucleotide-coated latex beads can be injected into cells and will be efficiently transported into cells after the beads initiate endocytosis, thus increasing gene transfer and expression efficiency. This method can be improved further by treating the beads to increase their hydrophobicity, thereby facilitating the disruption of the endosome and release of *hPNQALRE* subgenomic polynucleotides into the cytoplasm.

hPNQALRE may interact with different cyclins to achieve different effects within a cell. For example, cyclins which bind to hPNQALRE may function to regulate transcription. Cyclins which bind to hPNQALRE can be identified using screens such as the yeast two-hybrid assay. This assay is described *inter alia* in Fields & Song, *Nature* *340*:245-46, 1989.

hPNQALRE mRNA is over-expressed in tumors compared with *hPNQALRE* mRNA expression levels in normal tissue. According to the present invention, tumors can be treated by contacting the tumor with a composition which can decrease the level of functional hPNQALRE protein in the tumor, for example, by decreasing levels of hPNQALRE or by blocking or reducing its function. Neoplasias which can be treated

include, but are not limited to, colorectal carcinomas, melanomas, squamous cell carcinomas, adenocarcinomas, hepatocellular carcinomas, renal cell carcinomas, sarcomas, myosarcomas, non-small cell lung carcinomas, leukemias, lymphomas, osteosarcomas, central nervous system tumors such as gliomas, astrocytomas, oligodendrogliomas, and neuroblastomas, breast tumors, tumors of mixed origin, such as Wilms' tumor and teratocarcinomas, and metastatic tumors. Proliferative disorders, such as anhydric hereditary ectodermal dysplasia, congenital alveolar dysplasia, epithelial dysplasia of the cervix, fibrous dysplasia of bone, and mammary dysplasia, can also be treated according to the invention. Hyperplasias, for example, endometrial, adrenal, breast, prostate, or thyroid hyperplasias, or pseudoepitheliomatous hyperplasia of the skin can also be treated according to the present invention.

The composition comprises a reagent which specifically binds to an *hPNQALRE* expression product so as to decrease the level of functional hPNQALRE protein in a cell, such as a tumor cell. In one embodiment of the invention, the reagent is a ribozyme, an RNA molecule with catalytic activity. *See, e.g.*, Cech, *Science 236*: 1532-1539; 1987; Cech, *Ann. Rev. Biochem. 59*:543-568; 1990, Cech, *Curr. Opin. Struct. Biol. 2*: 605-609; 1992, Couture and Stinchcomb, *Trends Genet. 12*: 510-515, 1996. Ribozymes can be used to inhibit gene function by cleaving an RNA sequence, as is known in the art (*e.g.*, Haseloff *et al.*, U.S. Patent 5,641,673).

A coding sequence of an *hPNQALRE* gene can be used to generate ribozymes which will specifically bind to mRNA transcribed from the *hPNQALRE* gene. Methods of designing and constructing ribozymes which can cleave other RNA molecules in trans in a highly sequence specific manner have been developed and described in the art (*see* Haseloff *et al. Nature 334*:585-591, 1988). For example, the cleavage activity of ribozymes can be targeted to specific *hPNQALRE* RNAs by engineering a discrete "hybridization" region into the ribozyme. The hybridization region contains a sequence complementary to the target *hPNQALRE* RNA and thus specifically hybridizes with the target (see, for example, Gerlach *et al.*, EP 321,201). The nucleotide sequences shown in SEQ ID NOS:1, 3, 5, and 7 provide sources of suitable hybridization region sequences. Preferred ribozyme "hybridization" regions comprise in whole or in part nucleotides 76-114 of SEQ ID NO:5 or SEQ ID NO:7. Other preferred ribozyme

"hybridization" regions comprise in whole or in part nucleotides 503-564 of SEQ ID NO:3 or nucleotides 542-603 of SEQ ID NO:5 or SEQ ID NO:7. Longer complementary sequences can be used to increase the affinity of the hybridization sequence for the target. The hybridizing and cleavage regions of the *hPNQALRE* ribozyme can be integrally related; thus, upon hybridizing to the target *hPNQALRE* RNA through the complementary regions, the catalytic region of the ribozyme can cleave the target.

hPNQALRE ribozymes can be introduced into cells as part of a construct, as is known in the art and described above. Mechanical methods, such as microinjection, liposome-mediated transfection, electroporation, or calcium phosphate precipitation, can be used to introduce the ribozyme-containing construct into cells in which it is desired to decrease *hPNQALRE* expression, as described above. Alternatively, if it is desired that the cells stably retain the construct, it can be supplied on a plasmid and maintained as a separate element or integrated into the genome of the cells, as is known in the art. The construct can include transcriptional regulatory elements, such as a promoter element, an enhancer or UAS element, and a transcriptional terminator signal, for controlling transcription of *hPNQALRE* ribozymes in the cells.

In another embodiment of the invention, the level of hPNQALRE protein is decreased using an antisense oligonucleotide sequence. The antisense sequence is complementary to at least a portion of a sequence encoding hPNQALRE selected from the nucleotide sequences shown in SEQ ID NOS:1, 3, 5, and 7. Preferably, the antisense oligonucleotide sequence is at least 11 nucleotides in length, but can be at least 12, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides long. More preferably, antisense oligonucleotide sequences of 11, 12, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides are complementary to nucleotides 76-114 of SEQ ID NO:5 and SEQ ID NO:7 or are complementary to nucleotides 503-564 of SEQ ID NO:3 or nucleotides 542-603 of SEQ ID NO:5 or SEQ ID NO:7. Longer sequences can also be used. *hPNQALRE* antisense oligonucleotide molecules can be provided in a construct and introduced into cells as disclosed herein to decrease the level of functional hPNQALRE protein in the cells.

hPNQALRE antisense oligonucleotides can be deoxyribonucleotides, ribonucleotides, or a combination of both. Oligonucleotides can be synthesized manually or by an automated synthesizer, by covalently linking the 5' end of one nucleotide with the 3' end of another nucleotide with non-phosphodiester internucleotide linkages such alkylphosphonates, phosphorothioates, phosphorodithioates, alkylphosphonothioates, alkylphosphonates, phosphoramidates, phosphate esters, carbamates, acetamidate, carboxymethyl esters, carbonates, and phosphate triesters. *See* Brown, *Meth. Mol. Biol. 20*:1-8, 1994; Sonveaux, *Meth. Mol. Biol. 26*:1-72, 1994; Uhlmann *et al.*, *Chem. Rev. 90*:543-583, 1990.

Precise complementarity is not required for successful duplex formation between an antisense molecule and the complementary coding sequence of an *hPNQALRE* gene. Antisense molecules which comprise, for example, 2, 3, 4, or 5 or more stretches of contiguous nucleotides which are precisely complementary to an *hPNQALRE* coding sequence, each separated by a stretch of contiguous nucleotides which are not complementary to adjacent *hPNQALRE* coding sequences, can provide targeting specificity for *hPNQALRE* mRNA. Preferably, each stretch of contiguous nucleotides is at least 4, 5, 6, 7, or 8 or more nucleotides in length. Non-complementary intervening sequences are preferably 1, 2, 3, or 4 nucleotides in length. One skilled in the art can easily use the calculated melting point of an antisense-sense pair to determine the degree of mismatching which will be tolerated between a particular antisense oligonucleotide and a particular *hPNQALRE* coding sequence.

hPNQALRE antisense oligonucleotides can be modified without affecting their ability to hybridize to an *hPNQALRE* coding sequence. These modifications can be internal or at one or both ends of the antisense molecule. For example, internucleoside phosphate linkages can be modified by adding cholesteryl or diamine moieties with varying numbers of carbon residues between the amino groups and terminal ribose. Modified bases and/or sugars, such as arabinose instead of ribose, or a 3', 5'-substituted oligonucleotide in which the 3' hydroxyl group or the 5' phosphate group are substituted, can also be employed in a modified antisense oligonucleotide. These modified oligonucleotides can be prepared by methods well known in the art. *See, e.g.*, Agrawal

et al., *Trends Biotechnol. 10*:152-158, 1992; Uhlmann *et al.*, *Chem. Rev. 90*:543-584, 1990; Uhlmann *et al.*, *Tetrahedron. Lett. 215*:3539-3542, 1987.

Antibodies of the invention which specifically bind to hPNQALRE epitopes, particularly to the cyclin binding domain of hPNQALRE, can also be used to alter levels of functional hPNQALRE protein, by binding to hPNQALRE protein and decreasing the level of hPNQALRE protein which can function in the cell. Polynucleotides encoding single-chain antibodies of the invention can be introduced into cells as described above.

Preferably, the mechanism used to decrease the level of functional hPNQALRE in a cell decreases the level of functional hPNQALRE protein by at least 50%, 60%, 70%, or 80%. Most preferably, the level of functional hPNQALRE protein is decreased by at least 90%, 95%, 99%, or 100%. The effectiveness of the mechanism chosen to decrease the level of functional hPNQALRE protein can be assessed using methods well known in the art, such as hybridization of nucleotide probes to *hPNQALRE* mRNA, quantitative RT-PCR, detection of hPNQALRE protein using hPNQALRE-specific antibodies of the invention, or measurement of cyclin-dependent kinase activity. Assays for cyclin-dependent kinase activity are taught, for example, in Lock *et al.*, 1997, *Cancer Chemother. Pharmacol. 39*:399-409.

Compositions comprising hPNQALRE antibodies, ribozymes, or antisense oligonucleotides can optionally comprise a pharmaceutically acceptable carrier. Pharmaceutically acceptable carriers are well known to those in the art. Such carriers include, but are not limited to, large, slowly metabolized macromolecules, such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Pharmaceutically acceptable salts can also be used in hPNQALRE compositions, for example, mineral salts such as hydrochlorides, hydrobromides, phosphates, or sulfates, as well as salts of organic acids such as acetates, proprionates, malonates, or benzoates. hPNQALRE compositions can also contain liquids, such as water, saline, glycerol, and ethanol, as well as substances such as wetting agents, emulsifying agents, or pH buffering agents. Liposomes, such as those described in U.S. Patent 5,422,120, WO 95/13796, WO 91/14445, or EP 524,968 B1, can also be used as a carrier for an hPNQALRE composition.

Typically, an hPNQALRE composition is prepared as an injectable, either as a liquid solution or suspension; however, solid forms suitable for solution or suspension in liquid vehicles prior to injection can also be prepared. An hPNQALRE composition can also be formulated into an enteric coated tablet or gel capsule according to known methods in the art, such as those described in U.S. Patent 4,853,230, EP 225,189, AU 9,224,296, and AU 9,230,801.

Administration of hPNQALRE compositions of the invention can include local or systemic administration, including injection, oral administration, particle gun, or catheterized administration, and topical administration. Various methods can be used to administer an hPNQALRE composition directly to a specific site in the body. For inducing apoptosis in a tumor, for example, an appropriate hPNQALRE composition injected several times in several different locations within the body of the tumor. Alternatively, arteries which serve the tumor can be identified, and an hPNQALRE composition can be injected into such an artery in order to deliver the composition to the tumor.

A tumor which has a necrotic center can be aspirated, and an hPNQALRE composition can be injected directly into the now empty center of the tumor. An hPNQALRE composition can also be administered directly to the surface of a tumor, for example, by topical application of the composition. X-ray imaging can be used to assist in certain of these delivery methods. Combination therapeutic agents, including an hPNQALRE-specific antibody, ribozyme, or oligonucleotide or a subgenomic *hPNQALRE* polynucleotide encoding an hPNQALRE-specific antibody, ribozyme, or oligonucleotide, can be administered simultaneously or sequentially together with other therapeutic agents.

hPNQALRE compositions can be delivered to specific tissues using receptor-mediated targeted delivery. Receptor-mediated DNA delivery techniques are taught in, for example, Findeis *et al. Trends in Biotechnol. 11*, 202-05, (1993); Chiou *et al.*, GENE THERAPEUTICS: METHODS AND APPLICATIONS OF DIRECT GENE TRANSFER (J.A. Wolff, ed.) (1994); Wu & Wu, *J. Biol. Chem. 263*, 621-24, 1988; Wu *et al., J. Biol. Chem. 269*, 542-46, 1994; Zenke *et al., Proc. Natl. Acad. Sci. U.S.A. 87*, 3655-59, 1990; Wu *et al., J. Biol. Chem. 266*, 338-42, 1991.

Both the dose of a particular hPNQALRE composition and the means of administering the composition can be determined based on specific qualities of the hPNQALRE composition, the condition, age, and weight of the patient, the progression of the particular disease being treated, and other relevant factors. If the composition contains hPNQALRE antibodies, effective dosages of the composition are in the range of about 5 μg to about 50 mg/kg of patient body weight, about 50 μg to about 5 mg/kg, about 100 μg to about 500 μg/kg of patient body weight, and about 200 to about 250 μg/kg.

Compositions containing *hPNQALRE* subgenomic polynucleotides, including antisense oligonucleotides and ribozyme-or antibody-encoding sequences, can be administered in a range of about 100 ng to about 200 mg of DNA for local administration. Suitable concentrations range from about 500 ng to about 50 mg, about 1 μg to about 2 mg, about 5 μg to about 500 μg, and about 20 μg to about 100 μg of DNA. Factors such as method of action and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy of the hPNQALRE composition. If greater expression is desired over a larger area of tissue, larger amounts of an hPNQALRE composition or the same amount administered successively, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect.

Expression of an endogenous *hPNQALRE* gene in a cell can be altered by introducing in frame with the endogenous *hPNQALRE* gene a DNA construct comprising an *hPNQALRE* targeting sequence, a regulatory sequence, an exon, and an unpaired splice donor site by homologous recombination, such that a homologously recombinant cell comprising a new *hPNQALRE* transcription unit is formed. The new transcription unit can be used to turn the *hPNQALRE* gene on or off as desired. This method of affecting endogenous gene expression is taught in U.S. Patent 5,641,670.

The targeting sequence is a segment of at least 10, 12, 15, 20, or 50 contiguous nucleotides selected from a nucleotide sequence shown in SEQ ID NOS:1, 3, 5, or 7. Preferred targeting sequences are selected from nucleotides 76-114 of SEQ ID NO:5

and SEQ ID NO:7 as well as from nucleotides 503-564 of SEQ ID NO:3 or nucleotides 542-603 of SEQ ID NO:5 or SEQ ID NO:7. The new transcription unit is located upstream of a coding sequence of the endogenous *hPNQALRE* gene. The exogenous regulatory sequence directs transcription of the coding sequence of the *hPNQALRE* gene.

The invention also provides a method of diagnosing or prognosing neoplasia in a mammal, preferably a human. Expression of an *hPNQALRE* gene in a first tissue suspected of being neoplastic can be compared with expression of an *hPNQALRE* gene in a second tissue which is normal. The *hPNQALRE* gene can have a coding sequence as shown in SEQ ID NOS:1, 3, 5, or 7. Preferably, the *hPNQALRE* gene will comprise nucleotides 76-114 of SEQ ID NO:5 and SEQ ID NO:7 and/or nucleotides 503-564 of SEQ ID NO:3 or nucleotides 542-603 of SEQ ID NO:5 or SEQ ID NO:7.

Comparisons can be made, for example, by measuring levels of *hPNQALRE* mRNA or hPNQALRE protein in the first and second tissues, as is known in the art. The first and second tissues can originate from the same subject or from different subjects. The first and second tissues can be of different types, but are preferably from the same type of tissue, such as an intestinal polyp. Alternatively, standard curves of *hPNQALRE* gene expression can be determined from a number of normal tissue samples and used for comparison with *hPNQALRE* gene expression in a tissue suspected of being neoplastic.

Over-expression of the *hPNQALRE* gene in the first tissue compared with *hPNQALRE* gene expression in the second tissue or the standard curve indicates neoplasia in the first tissue. Levels of over-expression can correlate with stages of neoplasia and can be used, for example, to monitor treatment of a patient, preferably a human patient.

An *hPNQALRE* subgenomic polynucleotide can also be delivered to subjects for the purpose of screening test compounds for those which are useful for enhancing transfer of *hPNQALRE* subgenomic polynucleotides to the cell or for enhancing subsequent biological effects of *hPNQALRE* subgenomic polynucleotides within the cell. Such biological effects include hybridization to complementary *hPNQALRE* mRNA and inhibition of its translation, expression of an *hPNQALRE* subgenomic

polynucleotide to form an *hPNQALRE* mRNA, single-chain antibody, ribozyme, oligonucleotide, or protein and/or hPNQALRE and replication and integration of an *hPNQALRE* subgenomic polynucleotide. The subject can be a cell culture or an animal, preferably a mammal, more preferably a human.

Test compounds which can be screened include any substances, whether natural products or synthetic, which can be administered to the subject *in vitro* or *in vivo*. Libraries or mixtures of compounds can be tested. The compounds or substances can be those for which a pharmaceutical effect is previously known or unknown. The compounds or substances can be delivered before, after, or concomitantly with an *hPNQALRE* subgenomic polynucleotide. They can be administered separately or in admixture with an *hPNQALRE* subgenomic polynucleotide.

Integration of a delivered hPNQALRE subgenomic polynucleotide can be monitored by any means known in the art. For example, Southern blotting of the delivered *hPNQALRE* subgenomic polynucleotide can be performed. A change in the size of the fragments of a delivered polynucleotide indicates integration. Replication of a delivered polynucleotide can be monitored *inter alia* by detecting incorporation of labeled nucleotides combined with hybridization to an *hPNQALRE* probe. Expression of an *hPNQALRE* subgenomic polynucleotide can be monitored by detecting production of *hPNQALRE* mRNA which hybridizes to the delivered polynucleotide or by detecting hPNQALRE protein. hPNQALRE protein can be detected immunologically. Thus, the delivery of *hPNQALRE* subgenomic polynucleotides according to the present invention provides an excellent system for screening test compounds for their ability to enhance transfer of *hPNQALRE* polynucleotides to a cell, by enhancing delivery, integration, hybridization, expression, replication or integration in a cell *in vitro* or *in vivo* in an animal, preferably a mammal, more preferably a human.

The complete contents of all references cited in this disclosure are expressly incorporated by reference herein. The following are provided for exemplification purposes only and are not intended to limit the scope of the invention which has been described in broad terms above.

EXAMPLES

This example demonstrates expression of *hPNQALRE* mRNA in human tissues and cell lines.

Northern blots of human heart, brain, placenta, lung, liver, muscle, kidney, pancreas, spleen, thymus, prostate, testis, ovary, small intestine, colon, and peripheral blood lymphocytes were assayed for *hPNQALRE* expression. The cell lines HL-60, HeLa, Molt-4, K565, Raji, SW480, A549, and G361 were also assayed for *hPNQALRE* mRNA expression.

hPNQALRE mRNA is expressed in most tissues at very low levels. Expression was most pronounced in brain, pancreas, testis, and ovary. In contrast, *hPNQALRE* mRNA was expressed at higher levels in cancer cell lines. Expression of *hPNQALRE* mRNA was highest in the cell lines K565, A549, G361, and SW480.

These results indicate that *hPNQALRE* is over-expressed in cancer cell lines compared with expression levels in the corresponding normal tissues.

EXAMPLE 2

This example describes distribution of *hPNQALRE* mRNA in developing mouse embryos.

Mouse embryos were processed for whole-mount *in situ* hybridization as described in Lyn, S. D., "Whole-mount *in situ* hybridization of mouse embryos exposed to teratogenic levels of retinoic acid," *Meth. Mol. Biol.*, *89*:67-69, 1998, and Nieto et al., "*In situ* hybridization analysis of chick embryos in whole mount and tissue sections," *Meth. Cell Biol.*, *51*:219-35, 1996. *In situ* hybridization on whole mount embryos indicated that *hPNQALRE* mRNA is expressed overall in embryonic tissue, particularly in the developing limbs.

These results indicate that *hPNQALRE* may become differentially expressed in particular tissues over the course of embryonic development.

EXAMPLE 3

This example demonstrates the generation of polyclonal antibodies against hPNQALRE.

Rabbits were immunized with a peptide fragment of hPNQALRE with the sequence N-HDFHVDRPLEESLINPELIRP-C (SEQ ID NO:17) coupled to keyhole limpet hemocyanin. A preparation of polyclonal antibodies was generated which recognized hPNQALRE protein expressed from COS and U87 cells.

These results demonstrate that hPNQALRE polypeptide fragments can be used as immunogens.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All patents, published patent applications, and publications cited herein are incorporated by reference as if set forth fully herein.